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<!--StartFragment-->Q9XE52_ARATH
ID   Q9XE52_ARATH  PRELIMINARY;   PRT;   325 AA.
AC   Q9XE52;
DT   01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Scarecrow-like 3 (Fragment).
GN   Name=SCL3;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99272994; PubMed=10341448;
RA   Pysh L.D., Wysocka-Diller J.W., Camilleri C., Bouchez D., Benfey P.N.;
RT   "The GRAS gene family in Arabidopsis: sequence characterization and
RT   basic expression analysis of the SCARECROW-LIKE genes.";
RL   Plant J. 18:111-119 (1999).
CC   -----
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CC   -----
DR   EMBL; AF036301; AAD24404.1; -; mRNA.
DR   PIR; T51235; T51235.
DR   InterPro; IPR005202; GRAS.
DR   Pfam; PF03514; GRAS; 1.
DR   PROSITE; PS0985; GRAS; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      325 AA;  36718 MW;  136E843F20E7989F CRC64;

Query Match      68.2%; Score 1697; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.1e-115;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      158 AMEGEKMHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGVHHQKEVLEQMAHRLIEE 217
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Db      1 AMEGEKMHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGVHHQKEVLEQMAHRLIEE 60

Qy      218 AEKLDIPFPQFNFPVSRDLCLNVEQLRVKTGEALAVSSVLQLHTFLASDDDLMRKNALRF 277
      |||
Db      61 AEKLDIPFPQFNFPVSRDLCLNVEQLRVKTGEALAVSSVLQLHTFLASDDDLMRKNALRF 120

Qy      278 QNPNPSGVDLQRVLMMSHGSAEARENDMSNNNGYSPSGDSASSLPLSSGRTDSFLNAIW 337
      |||
Db      121 QNPNPSGVDLQRVLMMSHGSAEARENDMSNNNGYSPSGDSASSLPLSSGRTDSFLNAIW 180

Qy      338 GLSPKVMVVTEQSDHNGSTLMERLLESYTYAALFDCLETKVPRTSQDRIKVEKMLFGE 397
      |||
Db      181 GLSPKVMVVTEQSDHNGSTLMERLLESYTYAALFDCLETKVPRTSQDRIKVEKMLFGE 240

Qy      398 EIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYIAMLQARRLLQCGGFDGYRIK 457
      |||
Db      241 EIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYIAMLQARRLLQCGGFDGYRIK 300

Qy      458 EESGCAVICWQDRPLYSVSAWRCRK 482
      |||
Db      301 EESGCAVICWQDRPLYSVSAWRCRK 325
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